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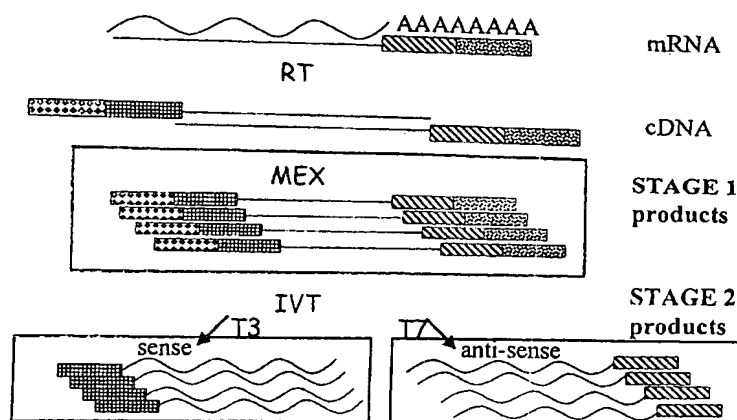
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(54) Title: NUCLEIC ACID AMPLIFICATION METHOD



(57) Abstract: A method for increasing the number of polynucleotides containing sequences corresponding to a mRNA species present in a sample, comprises the steps of: (i) reverse transcription of the mRNA species using a heeled 5'-amplification primer (FAP-RAND) and a heeled 3'-amplification primer (TAP-RT), wherein each primer sequence is unique, and either or each heel sequence includes a RNA polymerase promoter site, and the FAP includes a variable sequence, whereby the RNA is reverse-transcribed to produce double-stranded cDNA and then multiple cDNAs according to the variable sequence; and (ii) amplification of the cDNA using primers sufficiently complementary to the primers, i.e. FAP and TAP, within FAP-RAND and TAP-RT. In one embodiment, the method additionally comprises the step of: (iii) *in vitro* transcription, to produce RNA run-offs from either end of the amplicons.

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INTERNATIONAL SEARCH REPORT

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 A. CLASSIFICATION OF SUBJECT MATTER
 IPC 7 C12Q1/68 C12N15/10

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B. FIELDS SEARCHED

 Minimum documentation searched (classification system followed by classification symbols)
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Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

 Electronic data base consulted during the international search (name of data base and, where practical, search terms used)
 EPO-Internal, WPI Data, PAJ, EMBASE, BIOSIS

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 01 06004 A (UNIV CAMBRIDGE TECH; COX PETER (GB); RICHARDSON PETER (GB)) 25 January 2001 (2001-01-25) cited in the application the whole document	1-15, 17, 18
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☒ Patent family members are listed in annex.

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